

Tue Aug 28 11:09:18 2001

us-09-486-334-2.rsp

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: August 21, 2001, 12:06:43 ; Search time 11.18 Seconds
(without alignments)
962.095 Million cell updates/sec

Title: us-09-486-334-2
Perfect score: 1641
Sequence: 1 MATCIDTCRTGNTODDSRF.....IPCLTMDQSYLTMSDYVI 314

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 93435 segs, 3425486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	648.5	39.5	273	1	CYSE_ECOLI P05796 escherichia
2	648.5	39.5	273	1	CYSE_SALTY P29847 salmonella
3	624.5	38.1	267	1	CYSE_HAETN P43866 haemophilus
4	573.5	34.9	274	1	CYSE_BUCAL P32003 buchnera ap
5	549.5	33.5	261	1	CYSE_BUCAL P06002 buchnera ap
6	430.5	28.2	244	1	CYSE_SYNP7 P06750 bacillus su
7	424	25.8	217	1	CYSE_BACSU P74089 synecocyst
8	420.5	25.6	249	1	CYSE_SYNP3 P77985 staphylococ
9	399	24.3	216	1	CYSE_STAXY P23145 staphylococ
10	369.5	22.5	269	1	CYSE_HELPY P71405 helicobacte
11	365	22.2	171	1	CYSE_HELPY P71405 helicobacte
12	359	21.9	171	1	CYSE_HELPY P71405 helicobacte
13	287	17.5	319	1	SRPH_SYNP7 P77558 escherichia
14	217	13.2	162	1	WCAB_ECOLI P08632 rhizobium l
15	164.5	10.0	190	1	NODL_RHILV P05846 methanococ
16	164.5	10.0	214	1	YAG4_METUA P07464 escherichia
17	160	9.8	203	1	THGA_ECOLI P40892 saccharomyc
18	156.5	9.5	196	1	YJY8_YEAST P09707 schizosacch
19	153.5	9.4	207	1	YJY8_YEAST P28266 rhizobium m
20	150	9.1	183	1	YJY8_YEAST P28266 rhizobium m
21	146.5	8.9	346	1	YJY8_YEAST P28266 rhizobium m
22	136.5	8.3	184	1	YJY8_YEAST P28266 rhizobium m
23	133.5	8.1	345	1	YJY8_YEAST P28266 rhizobium m
24	127.5	7.9	182	1	YJY8_YEAST P28266 rhizobium m
25	127.5	7.8	261	1	YJY8_YEAST P28266 rhizobium m
26	126.5	7.7	172	1	YJY8_YEAST P28266 rhizobium m
27	126.5	7.3	207	1	YJY8_YEAST P28266 rhizobium m
28	120.5	7.3	159	1	YJY8_YEAST P28266 rhizobium m
29	120	7.2	182	1	YJY8_YEAST P28266 rhizobium m
30	117.5	7.0	267	1	YJY8_YEAST P28266 rhizobium m
31	115.5	7.0	262	1	YJY8_YEAST P28266 rhizobium m
32	115	7.0	262	1	YJY8_YEAST P28266 rhizobium m
33	114.5	7.0	262	1	YJY8_YEAST P28266 rhizobium m

RESULT	ID	STANDARD	PRT
34	112.5	6.9	456
35	112	6.8	116
36	112	6.8	456
37	110	6.7	209
38	110	6.6	456
39	106.5	6.5	341
40	105.5	6.4	171
41	104.5	6.4	275
42	103.5	6.3	209
43	103	6.3	210
44	103	6.3	210
45	102.5	6.2	210

ALIGNMENTS

RESULT 1
ID CYSE_ECOLI STANDARD: PRT: 273 AA.
AC P05796:
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
OS Escherichia coli.
GN Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88009872; PubMed=3309158;
RA Deak D., Boeck A.;
RT "L-cysteine biosynthesis in Escherichia coli: nucleotide sequence and expression of the serine acetyltransferase (cysE) gene from the wild-type and a cysteine-excreting mutant."
RT J. Gen. Microbiol. 133:515-525(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90211342; PubMed=2108679;
RA Tel H., Murata K., Kimura A.;
RT "Structure and expression of cysX, the second gene in the Escherichia coli K-12 cys locus."
RT Biochem. Biophys. Res. Commun. 167:948-955(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes."
RT Nucleic Acids Res. 22:2576-2586(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=91099514; PubMed=2125278;
RA Wigley D.B., Derrick J.P., Shaw W.V.;
RT "The serine acetyltransferase from Escherichia coli: over-expression, purification and preliminary crystallographic analysis."
RT FEBS Lett. 277:267-271(1990).
RN [5]
RP SUBUNIT.
RX MEDLINE=20085066; PubMed=10617639;
RA Hinton V.J., Moody P.C., Rowe A.J., Shaw W.V.;
RT "Serine acetyltransferase from Escherichia coli is a dimer of trimers."
RX J. Biol. Chem. 275:461-466(2000).
CC -I- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
CC -I- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
CC -I- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -I- SUBUNIT: HOMODIMER. DIMER OF A HOMOTRIMER.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC
 DR EMBL: M15745; AAA33648.1;
 DR EMBL: M34333; AAA23659.1;
 DR EMBL: U00039; AAB18584.1;
 DR PIR: A27896; XECSA.
 DR PIR: A34563; A34563.
 DR ECODBASE: H029.3; 6TH EDITION.
 DR Ecogene: EGI0187; CYSE.
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep. 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 DR Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 KW SEQUENCE 273 AA; 29316 MW; 466EB898750EF709 CRC64;
 SQ

Query Match
 Best Local Similarity 39.5%; Score 648.5; DB 1; Length 273;
 Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

DB 4 EELEIYWNKIKAEKADVKOEPIISNYVYASITSHRSLSALAHILSVKLSNLPNTL 102
 QY 103 FEFIFVLESESEITESTKODLAVKERDPACISYHCEFLKGFACQARHIAHTLMO 63
 DB 64 REVEEAAYADPEMIASACDIOAVTRDPADVKTSTPLLYLKGFHALQVRIHMLNQ 162
 QY 163 NKRIYALLIONRSEFAVDIHFGAKIGKGLIDHATGVIGVAVGVNDVSTILHGYTLG 123
 DB 124 GRRAIAIFLQNOVSFQVDIHPAKIGRGIMLDHATGIVGETAVIDENSTLQSVTLG 222
 QY 223 GTGKSGDRHPIKIGDVLIGAGSCILGNTTIGEGAKIGSGSVVKKDVPARTAVGNPRL 183
 DB 184 GTGKSGDRHPIKIGDVLIGAGSCILGNTTIGEGAKIGSGSVVKKDVPARTAVGNPRL 282
 QY 283 IGGKENPKRHDKTICPLTMDQ 302
 DB 244 VGKPGS----DK-PSMDMDQ 258

RESULT 2
 CYSE_SALTY
 ID CYSE_SALTY STANDARD; PRT; 273 AA.
 AC P29847;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 GN SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 OS *Salmonella typhimurium*.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC *Salmonella*.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA SIVAPRASAD A.V., KUCZEK E.S., BAWDEN C.S., ROGERS G.E.;
 RN Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA ROGERS G.E.;

RT "Cysteine biosynthesis in transgenic animals."
 RL Patent number GB2227243, 25-JUL-1990.
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMODIMER. DIMER OF A HOMOTRIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC
 DR EMBL: X59594; CAA42163.1;
 DR EMBL: A00198; CAA00039.1;
 DR PIR: S29568; S29568.
 DR StyGene: SGI0073; CYSE.
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep. 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 DR Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 KW SEQUENCE 273 AA; 29291 MW; 6A5736E56FBD25B CRC64;
 SQ

Query Match
 Best Local Similarity 39.5%; Score 648.5; DB 1; Length 273;
 Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;

DB 4 EELEIYWNKIKAEKADVKOEPIISNYVYASITSHRSLSALAHILSVKLSNLPNTL 102
 QY 103 FEFIFVLESESEITESTKODLAVKERDPACISYHCEFLKGFACQARHIAHTLMO 63
 DB 64 REVEEAAYADPEMIASACDIOAVTRDPADVKTSTPLLYLKGFHALQVRIHMLNQ 162
 QY 163 NKRIYALLIONRSEFAVDIHFGAKIGKGLIDHATGVIGVAVGVNDVSTILHGYTLG 123
 DB 124 GRRAIAIFLQNOVSFQVDIHPAKIGRGIMLDHATGIVGETAVIDENSTLQSVTLG 222
 QY 223 GTGKSGDRHPIKIGDVLIGAGSCILGNTTIGEGAKIGSGSVVKKDVPARTAVGNPRL 183
 DB 184 GTGKSGDRHPIKIGDVLIGAGSCILGNTTIGEGAKIGSGSVVKKDVPARTAVGNPRL 282
 QY 283 IGGKENPKRHDKTICPLTMDQ 302
 DB 244 VGKPGS----DK-PSMDMDQ 258

RESULT 3
 CYSE_HAELN
 ID CYSE_HAELN STANDARD; PRT; 267 AA.
 AC P43886;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 GN SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 OS *Haemophilus influenzae*.
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC *Haemophilus*.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.B., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uiterback T.R., Hann M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.A., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd.,"
 RL Science 269:496-512(1995).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC -----
 CC EMBL: U32743; AAC2265.1; -.
 CC DR TIGR: H10606; -.
 CC DR InterPro: IPR001451; -.
 CC DR Pfam: PF00132; hexapep; 2.
 CC DR PROSITE: PS00101; HEXAPEP TRANSFERASES; 1.
 CC DR Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 CC KW SEQUENCE 267 AA; 29166 MW; 93428DE9D504DFB4 CRC64;
 SO
 Query Match 38.1%; Score 624.5; DB 1; Length 267;
 Best Local Similarity 48.4%; Pred. No. 2.4e-42; Indels 9; Gaps 2;
 Matches 125; Conservative 54; Mismatches 70;
 QY 47 DWIKMLEBAKDVKQEPITLSNYASITSRSLSALHLSVKLSNLPNTLFELEF 106
 DB 4 DWQOHTROKAEKLAENEPMLSEFSTILKHONGALSYLLANKLANIMPAISLREIT 63
 QY 107 ISVLESPETSTKODLIVAKERDPACISYVHCFLGFKGLCOAHRIATLMKONKRI 166
 DB 64 EBAYQSNPILIOACDIOAVRHDPVAVELMSTPLLYLKGHALQSRITHYIMNQNRKS 123
 QY 167 VALLIONRSESPANDVHPGAKIGKGLLDHATGVIGETAVGVNDVNSILHGTGLGCTK 226
 DB 124 LALYLQNOISVADVDPVHPAKIGKGLDHTATGVIGETAVGVNDVNSILHGTGLGCTK 183
 QY 227 QSGDRHKRIGDGVILGAGSCILGNTITGEGAKIGSGSVVVDVPAFTAVGNPARLIGCK 286
 DB 184 ESGDRHKRIGDGVILGAGSCILGNTITGEGAKIGSGSVVVDVPAFTAVGNPARLIGCK 240
 QY 287 ENPRKHDKI--PCLITMDQ 302
 DB 241 ----SODKARPAFDMQ 254
 RESULT 4
 CYSE_BUCAL STANDARD; PRT; 274 AA.
 AC P57162;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE OR BU054.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OC Bacterioidetes; Proteobacteria; gamma subdivision; Buchnera.
 NCBI_Taxid=118099;
 OX

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TORO 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS.,"
 RL Nature 407:81-86(2000).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC -----
 CC EMBL: AP001118; BAB1277.1; -.
 CC DR PROSITE: PS00101; HEXAPEP TRANSFERASES; 1.
 CC DR Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
 CC KW SEQUENCE 274 AA; 30165 MW; 553D252P1048B6B1 CRC64;
 SO
 Query Match 34.9%; Score 573.5; DB 1; Length 274;
 Best Local Similarity 48.9%; Pred. No. 2.0e-38; Indels 1; Gaps 1;
 Matches 116; Conservative 47; Mismatches 73;
 QY 48 VWIKMLEBAKDVKQEPITLSNYASITSRSLSALHLSVKLSNLPNTLFELEF 107
 DB 9 IWNKILYDVSEFLKKEITSDFYQSSILGHQSFSTLSYLSNKLSTSMSEKKIGCID 68
 QY 108 SVLESPETSTKODLIVAKERDPACISYVHCFLGFKGLCOAHRIATLMKONKRI 167
 DB 69 DYVINDRSLNFIYODIKAVLRDPVANDYLPPLLYLKGHALQSRITHYIMNQNRKS 128
 QY 168 VALLIONRSESPANDVHPGAKIGKGLLDHATGVIGETAVGVNDVNSILHGTGLGCTK 227
 DB 129 SHYLSRISSESVDPVHPAKIGKGLDHTATGVIGETAVGVNDVNSILHGTGLGCTK 188
 QY 228 -SGDRHKRIGDGVILGAGSCILGNTITGEGAKIGSGSVVVDVPAFTAVGNPARL 283
 DB 189 FSONRHPTIRKGVIGAGAKILGNIIEVGSAGKIGAGSVLVKPNPSVTVYVGPATIV 245
 RESULT 5
 CYSE_BUCAP STANDARD; PRT; 261 AA.
 ID CYSE_BUCAP
 AC P32003;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacterioidetes; Proteobacteria; gamma subdivision; Buchnera.
 NCBI_Taxid=98794;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93012960; PubMed=1398077;
 RA Lai C.-Y., Baumann P.;
 RT "Sequence analysis of a DNA fragment from Buchnera aphidicola (an
 RT endosymbiont of aphids) containing genes homologous to dnaG, ipod,
 RT cyse, and sebB.,"
 RL Gene 119:113-118(1992).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC DR EMBL: M90644; AAA73232.1;
 DR InterPro: JCI293; JCI293;
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP. TRANSFERASES; 1.
 DR TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 DR KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 DR SQ SEQUENCE 261 AA; 28914 MW; DC02685464A25944 CRC64;

Query Match
 Best Local Similarity 33.5%; Score 549.5; DB 1; Length 261;
 Matches 109; Conservative 53; Mismatches 84; Indels 1; Gaps 1;
 QY 47 DWIKLEAKSDVYKOEPIISNYYSITSHRLESALHILSVKLSNLPNTLPELF 106
 DB 8 ELMMNKKHAKOIKLEPIISNFOKSLNHNKLSHLSCLISDLSMTSEMDIYVIF 67
 QY 107 ISVLESEPIESTKODLIVKEDPACISYVCFEGFGLACQAHRIATITLKNKRT 166
 DB 68 NKIYANNISIIISVYKDIKASQSDPVVYKHYLPLLYLKPHALEVYLSHYLNIRYE 127
 QY 167 VALLIQRVSESAVDIHPGAKIGKGIILDHATGVYIETAVGDNVSIHLGVLGCTGK 226
 DB 128 LSAVLOSRISTVSVIHPAASIGSIMIDHATGVIEGVYIENDVSIHPSVTLGCTG 187
 QY 227 QSG-DRHPRKIGDVLIGAGSCITLNTTIGEGAKIGSGSVVYKVDVPAVTPVGPAPLIGG 285
 DB 188 NTGKNRPIIRKNTVITGAGAKILGNIIEVGQGVKAGSIVLKNIPVTVYVPAKTIKK 247
 QY 286 KENDRRH 292
 DB 248 IKNSMKN 254

RESULT 6
 CYSE_SYN7
 ID CYSE_SYN7 STANDARD; PRT; 244 AA.
 AC 056002;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE.
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 RX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96281517; PubMed=8661945;
 RA Anandan S., Nally M.S., Cogdell D.E., Golden S.S.;
 RT Identification of two classes of transcriptional regulator genes in
 RT the cyanobacterium Synechococcus sp. strain PCC 7942.
 RL Arch. Microbiol. 166:58-63(1996).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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 CC DR EMBL: M90644; AAA73232.1;
 DR InterPro: JCI293; JCI293;
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP. TRANSFERASES; 1.
 DR TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 DR KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 DR SQ SEQUENCE 261 AA; 28914 MW; DC02685464A25944 CRC64;

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 CC or send an email to license@isb-sib.ch).
 CC DR EMBL: I41665; AAB8543.1;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep; 2.
 DR PROSITE: PS00101; HEXAPEP. TRANSFERASES; 1.
 DR TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 DR KW TRANSFERASE; Acyltransferase; Cysteine biosynthesis; Repeat.
 DR SQ SEQUENCE 244 AA; 26453 MW; AB050491023EUB1 CRC64;

Query Match
 Best Local Similarity 26.2%; Score 430.5; DB 1; Length 244;
 Matches 85; Conservative 33; Mismatches 56; Indels 3; Gaps 1;
 QY 123 DLIAKEDPACISYVCFEGFGLACQAHRIATITLKNKRT 182
 DB 8 DERIFERDPARAGLEVLLCYRFGALVCHRYAHMLYQKUPVPRILSHLSRLTGE 67
 QY 183 IHPGAKIGKGIILDHATGVYIETAVGDNVSIHLGVLGCTGKSGDRPHKIGDVLG 242
 DB 68 IHPGAKIGKGIILDHATGVYIETAVGDNVSIHLGVLGCTGKSGDRPHKIGDVLG 242
 QY 243 AGSCITLNTTIGEGAKIGSGSVVYKVDVPAVTPVGPAPLIGG 296
 DB 128 AGAVLGNIDIGENVRIGAGSVLVDVPSDCTVYGIIFGVYVSGVAVPDLHSQMP 184

RESULT 7
 CYSE_BACSU
 ID CYSE_BACSU STANDARD; PRT; 217 AA.
 AC 006750;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
 GN CYSE OR CYSA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94171772; PubMed=7510287;
 RA Gagnon Y., Breton R., Putzer H., Pelchat M., Grunberg-Manago M.,
 RA Lapointe J.;
 RT Clustering and co-transcription of the Bacillus subtilis genes
 RT encoding the aminocyl-tRNA synthetases specific for glutamate and
 RT for cysteine and the first enzyme for cysteine biosynthesis.
 RL J. Biol. Chem. 269:7473-7482(1994).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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DR EMBL; M60090; AAA22162.1; -.

CC

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EMBL: U43917; AAB07027.1; -
EMBL: AE000626; AAD08254.1; -
DR TIGR; HP1210; -
DR InterPro; IPR001451; -
DR Pfam; PF00132; hexapep; 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
FT VARIANT 5 5 S -> F (IN STRAIN 60190).
FT VARIANT 110 110 K -> R (IN STRAIN 60190).
FT VARIANT 162 162 S -> T (IN STRAIN 60190).
SQ SEQUENCE 171 AA; 18342 MW; 28646D539C2250C3 CRC64;

Query Match 22.2%; Score 365; DB 1; Length 171;
Best Local Similarity 45.2%; Pred. No. 4.1e-22;
Matches 71; Conservative 31; Mismatches 55; Indels 0; Gaps 0;

127 VKERDPACISVHCFLEFGKFLACQAHRIAHITLTKONRKIVALLIONRVSESPAVDHPG 186
11 VLQEDPPAARNKWEVLLPYGTHALCYRLAHALKRREFTIATLALSQLARFTIGIEIHFG 70
187 AKIGKILLDHATGVIGETAVGDNVSLHGVTLGSTGSGDRHPRKIGDGVLIAGASC 246
71 AKIGRGLFIDHGMGVIGETIEIGDDVTIYHGVTLGSTGKFKGRHPTLGNRVVVGAGAK 130
247 ILGNITIGEGAKIGSGSVVAVKDPARTTAVGNPARLI 283
131 VLGAICVGDVRIKANAVVLSDLPTGSTAVGSAKAKTI 167

RESULT 12
CYSE_HELPJ STANDARD: PRT; 171 AA.
ID CYSE_HELPJ
AC 092K14;
DT 01-OCT-2000 (Rel. 40; Created)
DT 01-OCT-2000 (Rel. 40; Last sequence update)
DT 01-OCT-2000 (Rel. 40; Last annotation update)
DE SERINE ACETYLTANSFERRASE (EC 2.3.1.30) (SAT).
GN CYSE OR JHP1133.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCBI_TaxID=85963;
RX MEDLINE=9120557; PubMed=9923662;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Ulla-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori";
RT Nature 397:176-180(1999).
RL -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOFL FAMILY OF ACETYLTANSFERRASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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EMBL: AE001541; AAD06715.1; -
DR InterPro; IPR001451; -
DR Pfam; PF00132; hexapep; 4.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat.
SQ SEQUENCE 171 AA; 18354 MW; 2872B7539C3AC14A CRC64;

Query Match 21.9%; Score 359; DB 1; Length 171;
Best Local Similarity 44.6%; Pred. No. 1.2e-21;
Matches 70; Conservative 31; Mismatches 56; Indels 0; Gaps 0;

127 VKERDPACISVHCFLEFGKFLACQAHRIAHITLTKONRKIVALLIONRVSESPAVDHPG 186
11 VLQEDPPAARNKWEVLLPYGTHALCYRLAHALKRREFTIATLALSQLARFTIGIEIHFG 70
187 AKIGKILLDHATGVIGETAVGDNVSLHGVTLGSTGSGDRHPRKIGDGVLIAGASC 246
71 AKIGRGLFIDHGMGVIGETIEIGDDVTIYHGVTLGSTGKFKGRHPTLGNRVVVGAGAK 130
247 ILGNITIGEGAKIGSGSVVAVKDPARTTAVGNPARLI 283
131 VLGAICVGDVRIKANAVVLSDLPTGSTAVGSAKAKTI 167

RESULT 13
SRPH_SYN7 STANDARD: PRT; 319 AA.
ID SRPH_SYN7
AC 059967;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE SERINE ACETYLTANSFERRASE, PLASMIID (EC 2.3.1.30) (SAT).
GN SRPH.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
ON NCBI_TaxID=1140;
RX MEDLINE=95327059; PubMed=7603442;
RA Nicholson M.L., Gaasenbeek M., Landenbach D.E.;
RT "Two enzymes together capable of cysteine biosynthesis are encoded on a cyanobacterial plasmid";
RL Mol. Gen. Genet. 247:623-632(1995).
RL -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE.
CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOFL FAMILY OF ACETYLTANSFERRASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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EMBL: U23436; AAA86726.1; -
DR InterPro; IPR001451; -
DR Pfam; PF00132; hexapep; 2.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; FALSUNG.
KW Transferrase; Acyltransferase; Cysteine biosynthesis; Repeat; Plasmid.
SQ SEQUENCE 319 AA; 34570 MW; 00BB74D8AAB1170 CRC64;

Query Match 17.5%; Score 287; DB 1; Length 319;

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CC EMBL: U38473: AAC7837.1: -
DR

DR Ecogene; EG13570; wcab.
DR InterPro: IPR001451; -

162 AA: 17615 MW: 2346302.322 kDa: 23.46302322
SEQUENCE Lipopolysaccharide biosynthesis; Transferrase; Acyltransferase; Repeat.
KW Lipopolysaccharide biosynthesis; TRANSFERRASES; 1.
SO

Query Match	13.28;	Score 217;	DB 1;	Length 162;
Best Local Similarity	37.19;			
Best Word Similarity	37.19;			

QY 152 AHHIAH--TLWKQ-----NKKVALLIQRVSES--FAVDIHGAKIGKIGILLDHATGVV 202
11111

QY 203 IGETAVVGDNVSTLHGVTGGTGKQSGDRHPKIGDGVLTGACSCILGNITIGEGAKIGSG 262

QY 263 SYVVKDVPARTTAVGNPARL 282

ID	NODL_RHILV	STANDARD;	PRT;	190 AA.
AC	P08632;			

01-JUN-1994 (Rel. 29, Last annotation update)
DE MODULATION PROTEIN L (EC 2.3.1.-).

00C Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group.
00G Plasmid sym prLJI.

RN [1]
RP SEQUENCE FROM N.A.

Surin B.P., Downie J.A.;
"Characterization of the Rhizobium
leguminosarum ssp. caryum
PT

[2] SEQUENCE FROM N.A. RP 2.1.3 105(1508).

^aAdditional nodulation genes on the same plasmid as nif⁺: Wijnfelman C.A., Okker R.J.H., Lugtenberg B.J.J.; *Journal of General Microbiology*, 1987, 131, 1069-1074.

[3] SIMILARITY TO OTHER MEMBERS OF THE ORDER OF THE MONASTIC. *PLANT MOL. BIOL.* 13:103-114 (1989).

"The nodL gene from *Rhizobium leguminosarum* is homologous to the acetyl transferase encoded by the *acetyl* gene from *Escherichia coli*." *J. Biol. Chem.* 263: 1017-1020, 1988.

RL Mol. Microbiol. 3:1649-1651(1989).
 CC -1- FUNCTION: ACETYLTRANSFERASE IMPLICATED IN THE O-ACETYLATION OF
 CC NOD FACTORS.
 CC
 CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPYA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC
 CC -----
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 CC -----
 CC EMBL: X17557; CAA35590.1; -
 DR EMBL: Y00548; CAA68625.1; -
 DR PIR: S01039; S01039.
 DR PIR: S07000; S07000.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep. 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASE; Repeat.
 KW Plasmid; Modulation; Transferase; Acyltransferase; Repeat.
 SQ SEQUENCE 190 AA; 20105 MW; 2ACAAE82D6EDF48C CRC64;

Query Match 10.0%; Score 164.5; DB 1; Length 190;
 Best Local Similarity 42.7%; Pred. No. 3.1e-06;
 Matches 44; Conservative 13; Mismatches 39; Indels 7; Gaps 3;
 OY 193 ILDHATGVIGETAVVGDVNSIL-----HGVTLGGTGKSGDRHRPKIGDGVILGAGSCT 247
 DB 89 VILDYA-AVTIGDGTATGPAVQITADHPHDEQRQAGLQG--RPVSIGRHWANIGGAIL 146
 OY 248 LGNITIGEGAKIGSGVVVKDVPARTAVGNPARLIGKENPR 290
 DB 147 LPGVTIGDHAIVIGAGSVTRDVPAGSTAMGNPARVKAAGRLPK 189

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 Job time: 172 sec

